#3

SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Ciossek, Thomas
                                      Ullrich, Axel
                                      Millauer, Birgit

   (ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS
                                        AND TREATMENT OF MDK1
                                        SIGNAL TRANSDUCTION
                                        DISORDERS

  (iii) NUMBER OF SEQUENCES: 12

  (iv) CORRESPONDENCE ADDRESS:

        (A) ADDRESSEE: Lyon & Lyon
        (B) STREET: 633 West Fifth Street
                                        Suite 4700
        (C) CITY: Los Angeles
        (D) STATE: California
        (E) COUNTRY: U.S.A.
        (F) ZIP: 90071-2066

   (v) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                          storage
        (B) COMPUTER: IBM Compatible
        (C) OPERATING SYSTEM: IBM P.C. DOS 5.0
        (D) SOFTWARE: Word Perfect 5.1

  (vi) CURRENT APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/368,776
        (B) FILING DATE: January 3, 1995

        (C) CLASSIFICATION:

  (vii) PRIOR APPLICATION DATA:

Prior applications total,
including application
described below: none

    (A)   APPLICATION NUMBER:
    (B)   FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

    (A)   NAME: Warburg, Richard J.
    (B)   REGISTRATION NUMBER: 32,327
    (C)   REFERENCE/DOCKET NUMBER: 208/007

(ix) TELECOMMUNICATION INFORMATION:

    (A)   TELEPHONE: (213) 489-1600
    (B)   TELEFAX: (213) 955-0440
    (C)   TELEX: 67-3510

(2) INFORMATION FOR SEQUENCE ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:

    (A)   LENGTH: 4304 base pairs
    (B)   TYPE: nucleic acid
    (C)   STRANDNESS: single
    (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: nucleic

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA      50

CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG     100

GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA     150

TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACTG     200

CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACTCGG     250

TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA     300

CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG     350

CACAACAAAC AGAATTGGAA TGGATTTCCT CTCCACCCAG TGGGTGGGAA     400
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GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATACCAGGT   450

GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA   500

TTTCTAAAGG CAACGCACAA AGGATTTTTG TAGAATTGAA ATTCACCTTG   550

AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAACTTGCA AGGAAACGTT   600

TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG   650

AAAACCTTTA TGTTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA   700

CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA   750

GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCTTT CAGGATGTAG   800

GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG   850

ACCATTGTTG AGAACTTAGC TGTCTTTCCA GATACAGTGA CTGGTTCGGA   900

ATTTTCCTCC TTAGTCGAGG TCCGTGGGAC ATGTGTCAGC AGTGCCGAGG   950

AAGAGGCAGA AAATTCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG   1000

CTAGTACCCA TTGGAAAATG CATCTGCAAA GCAGGCTATC AGCAAAAAGG   1050

GGACACTTGC GAACCCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG   1100

ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA   1150

TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC   1200

ACCATACGTT GCATGCACGA GGCCTCCCTC TGCACCACAG AACCTTATTT   1250

TCAATATCAA TCAAACGACT GTAAGTTTGG AATGGAGTCC TCCGGCTGAC   1300

AACGGGGGAA GAAACGATGT CACCTACAGA ATACTGTGTA AGCGGTGCAG   1350

TTGGGAACAG GGAGAATGTG TGCCATGCGG AAGTAACATT GGATACATGC   1400

CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTCAT GGACCTACTT   1450

GCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCGGA   1500

CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGTC   1550

AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG   1600

CGGAGTGTGC AGCTTTCCTG GCAGGAGCCG GAGCATCCCA ATGGAGTCAT   1650

CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT   1700

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ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATTAA TAATCTGAAA    1750

CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGCCGGTTA    1800

TGGAAACTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG    1850

GTAAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCTGTCATC    1900

ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTCATGGT    1950

GTTCGGCTTC ATCATTGGAA GAAGGCACTG TGGTTATAGC AAGGCTGACC    2000

AAGAAGGGGA TGAAGAACTC TACTTTCATT TTAAATTTCC AGGCACCAAA    2050

ACCTACATTG ACCCTGAAAC CTATGAGGAC CCAAATAGAG CTGTCCATCA    2100

ATTCGCCAAG GAGCTAGATG CCTCCTGTAT TAAAATTGAG CGTGTGATTG    2150

GTGCAGGAGA ATTTGGAGAA GTTTGCAGTG GTCGTTTGAA ACTTCCGGGC    2200

CAGAGAGATG TTGCAGTGGC CATAAAAACC CTGAAAGTTG GTTACACAGA    2250

AAAGCAAAGG AGGGACTTTT TATGCGAAGC AAGCATCATG GGCAATTTG     2300

ACCACCCAAA TGTCGTCCAT TTGGAAGGGG TTGTTACAAG AGGGAAGCCT    2350

GTCATGATTG TGATAGAGTT CATGGAGAAT GGAGCCCTGG ATGCATTTCT    2400

CAGGAAACAC GATGGGCAGT TTACAGTCAT TCAGTTGGTA GGAATGTTGA    2450

GAGGTATTGC CGCTGGGATG CGATACTTGG CTGATATGGG ATACGTTCAC    2500

AGGGACCTTG CAGCGCGCAA CATCCTTGTC AACAGCAATC TTGTTTGTAA    2550

AGTGTCAGAT TTTGGCCTTT CCCGGGTTAT AGAGGATGAT CCCGAAGCTG    2600

TCTACACCAC GACTGGTGGA AAAATTCCAG TAAGGTGGAC TGCACCGGAA    2650

GCCATTCAAT ACCGGAAGTT CACCTCAGCC AGCGATGTGT GGAGCTATGG    2700

GATTGTCATG TGGGAAGTGA TGTCTTATGG AGAAAGACCT TACTGGGACA    2750

TGTCAAATCA AGATGTCATT AAAGCGATAG AAGAAGGTTA TCGTTTGCCG    2800

GCGCCCATGG ATTGCCCAGC TGGTCTTCAC CAGCTAATGC TGGATTGTTG    2850

GCAGAAAGAT CGGGCGGAAA GGCCAAAGTT TGAGCAGATA GTCGGAATTC    2900

TAGACAAAAT GATTCGAAAC CCAAGTAGTC TGAAAACACC CCTGGGAACT    2950

TGTAGTAGAC CCTTAAGCCC TCTTCTGGAC CAGAGCACTC CTGACTTCAC    3000
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TGCCTTCTGT TCAGTTGGAG AATGGTTGCA AGCTATTAAA ATGGAAAGGT 3050

ATAAGGACAA CTTCACAGCA GCGGGTTACA ACTCACTCGA GTCAGTGGCC 3100

AGGATGACTA TCGATGATGT GATGAGTTTA GGGATCACAC TGGTTGGCCA 3150

TCAAAAGAAG ATCATGAGCA GCATCCAGAC TATGCGGGCA CAAATGTTGC 3200

ATTTACACGG AACAGGCATC CAAGTGTGAC ACATCGGCCT CCCTCAGATG 3250

AGGCTTAAGA CTGCAGGAGA ACAGTTCTGG CCTTCAGTAT ACGCATAGAA 3300

TGCTGCTAGA AGACAGTTGA TATACTGGGT CCTTCCTACA AGAAAGAGAA 3350

GATTTTAGAA GCACCTCCAG ACTTGAACTC CTAAGTGCCA CCAGAATATA 3400

CAAAAAGGGA ATTTAGGATC CACCACTGGT GGCCAGGAAC ACAGCAGAGA 3450

CAATAAACAA AGTACTACCT GAAAAACATC CCAACACCTT GAGCTCTCGA 3500

ACCTCCTTTT TATCTTATAG ACTTTTTAAA AATGTACATA AAGAATTTAA 3550

GAAGAATAT ATTTGTCAAA TAAAAATCAT GATCTTATTG TTAAAATCAA 3600

TGAAATATTT TCCTTAAAAT ATGTGATTTC AGACTATTCT TTTCCAGAAC 3650

CATCTGTGTT TATTCTGCTT AAGGACTTTG TTTTAGAAAG TTATTTGTAG 3700

CTTTGGACCT TTTTAGTGTT AAATTTATGA CACGTTACTA CACTGGGAAC 3750

CTTTGAAGAC TCTCAAACTT AAAGGAAAGC AAAACTACGC ACATAGTCGA 3800

GGATGGACTT TGTCCTTCAT GGCTTTGGTA TCCTGGCTGT GTCATTTTGT 3850

TAAACCAGTG ATGTTTTCAT ATTGTTTGCT GATTGGCAGG TAGTTCAAAA 3900

TTGCAAGTTG CCAAGAGCTC TGATATTTTT TAACAGGATT TTTTTTTCTT 3950

TGTAAAAATC AGATAACATA CTAACTTTTC AATGAAAAAA AAAAAAAAG 4000

AAGCAATAAT GATCCATAAA TACTATAAGG CACTTTTAAC AGATTGTTTA 4050

TAGAGTGATT TACTAGGCAG AATTTAATAA AAAAAAAGA GAGATGTCAA 4100

ATTTTAGGTT TATGTGTATA TGATAAAGG CTGAGCTTCG TCTGAAGATG 4150

CTGGTGAAAG CAAGACTGGA AGCGAAGCTC TCCAGCTTTG GCTAACCCAA 4200

TCCGAGCACA TCAAGAGCTT CAGTCTTGTG ACAGTAAGAA ATTTAGGAAC 4250

ATAGTTGACC TATATTTTGT ATTCTTTCTT GTTGAATGCA GTCCAAATAC 4300

SSSD/27372. v01

AAAA   4304

(2)   INFORMATION FOR SEQUENCE ID NO: 2:

       (i)   SEQUENCE CHARACTERISTICS:

              (A)   LENGTH: 998 amino acids
              (B)   TYPE: amino acid
              (C)   STRANDNESS: single
              (D)   TOPOLOGY: linear

       (ii)   MOLECULE TYPE: peptide

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
1   5   10   15

Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
                20   25   30

Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
        35   40   45

Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
    50   55   60

Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
65   70   75   80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
            85   90   95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
            100   105   110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
        115   120   125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
    130   135   140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
145   150   155   160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
              165   170   175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
              180   185   190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
          195   200   205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
 210   215   220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
225   230   235   240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
              245   250   255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
              260   265   270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
          275   280   285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
      290   295   300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
305   310   315   320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
              325   330   335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
              340   345   350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
          355   360   365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
      370   375   380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
385   390   395   400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
              405   410   415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala

```
              420                    425                    430
Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
        435                440                445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
    450                455                460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
465                470                475                480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
            485                490                495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
        500                505                510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
    515                520                525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
530                535                540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
545                550                555                560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
            565                570                575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
            580                585                590

Asp Glu Glu Leu Tyr Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr
        595                600                605

Ile Asp Pro Glu Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe
    610                615                620

Ala Lys Glu Leu Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly
625                630                635                640

Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly
            645                650                655

Gln Arg Asp Val Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr
        660                665                670

Glu Lys Gln Arg Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln
        675                680                685
```

Phe Asp His Pro Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly
    690   695   700

Lys Pro Val Met Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp
705   710   715   720

Ala Phe Leu Arg Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val
          725   730   735

Gly Met Leu Arg Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met
          740   745   750

Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser
        755   760   765

Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu
    770   775   780

Asp Asp Pro Glu Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val
785   790   795   800

Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala
          805   810   815

Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr
        820   825   830

Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala
        835   840   845

Ile Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly
    850   855   860

Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg
865   870   875   880

Pro Lys Phe Glu Gln Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn
          885   890   895

Pro Ser Ser Leu Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser
        900   905   910

Pro Leu Leu Asp Gln Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val
        915   920   925

Gly Glu Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe
    930   935   940

Thr Ala Ala Gly Tyr Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile

```
945                      950                      955                      960
Asp Asp Val Met Ser Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys
                965                      970                      975
Ile Met Ser Ser Ile Gln Thr Met Arg Ala Gln Met Leu His Leu His
                980                      985                      990
Gly Thr Gly Ile Gln Val
        995
```

(2) INFORMATION FOR SEQUENCE ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 610 amino acids
        (B) TYPE: amino acid
        (C) STRANDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
1                5                   10                  15
Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
                20                  25                  30
Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
        35                  40                  45
Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
    50                  55                  60
Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
65                  70                  75                  80
Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
                85                  90                  95
Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
                100                 105                 110
Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
                115                 120                 125
```

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
130   135   140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
145   150   155   160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
165   170   175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
180   185   190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
195   200   205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
210   215   220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
225   230   235   240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
245   250   255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
260   265   270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
275   280   285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
290   295   300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
305   310   315   320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
325   330   335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
340   345   350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
355   360   365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
370   375   380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
385   390   395   400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
                405   410   415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
            420   425   430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
            435   440   445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
        450   455   460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
465   470   475   480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
                485   490   495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
            500   505   510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
            515   520   525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
    530   535   540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
545   550   555   560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
            565   570   575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
        580   585   590

Asp Glu Glu Leu Tyr Phe His Ser Leu Val Thr Asn Glu His Leu Ser
        595   600   605

Val Leu
610

(2)   INFORMATION FOR SEQUENCE ID NO: 4:

        (i)   SEQUENCE CHARACTERISTICS:

                (A)   LENGTH: 2901 base pairs
                (B)   TYPE: nucleic acid
                (C)   STRANDNESS: single

(D)   TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA      50

CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG     100

GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA     150

TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACTG     200

CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACTCGG     250

TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA     300

CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG     350

CACAACAAAC AGAATTGGAA TGGATTTCCT CTCCACCCAG TGGGTGGGAA     400

GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATACCAGGT     450

GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA     500

TTTCTAAAGG CAACGCACAA AGGATTTTTG TAGAATTGAA ATTCACCTTG     550

AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAACTTGCA AGGAAACGTT     600

TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG     650

AAAACCTTTA TGTTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA     700

CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA     750

GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCTTT CAGGATGTAG     800

GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG     850

ACCATTGTTG AGAACTTAGC TGTCTTTCCA GATACAGTGA CTGGTTCGGA     900

ATTTTCCTCC TTAGTCGAGG TCCGTGGGAC ATGTGTCAGC AGTGCCGAGG     950

AAGAGGCAGA AAATTCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG    1000

CTAGTACCCA TTGGAAAATG CATCTGCAAA GCAGGCTATC AGCAAAAAGG    1050

GGACACTTGC GAACCCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG    1100

ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA    1150
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TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC   1200

ACCATACGTT GCATGCACGA GGCCTCCCTC TGCACCACAG AACCTTATTT   1250

TCAATATCAA TCAAACGACT GTAAGTTTGG AATGGAGTCC TCCGGCTGAC   1300

AACGGGGGAA GAAACGATGT CACCTACAGA ATACTGTGTA AGCGGTGCAG   1350

TTGGGAACAG GGAGAATGTG TGCCATGCGG AAGTAACATT GGATACATGC   1400

CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTCAT GGACCTACTT   1450

GCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCGGA   1500

CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGTC   1550

AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG   1600

CGGAGTGTGC AGCTTTCCTG GCAGGAGCCG GAGCATCCCA ATGGAGTCAT   1650

CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT   1700

ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATTAA TAATCTGAAA   1750

CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGCCGGTTA   1800

TGGAAACTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG   1850

GTAAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCTGTCATC   1900

ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTCATGGT   1950

GTTCGGCTTC ATCATTGGAA GAAGGCACTG TGGTTATAGC AAGGCTGACC   2000

AAGAAGGGGA TGAAGAACTC TACTTTCATT CTTTAGTAAC AAATGAGCAC   2050

CTGTCAGTTT TATAAACCGC AACAATAACT GTTTAAGACA ATCAATTTTG   2100

GATAAACAAT CAACTACAGC AGAATAAATC AAGATTTTTA AGTCCCATTT   2150

TCCTTTATAC ATTCTGCTTA TTTTGTTGTT ATATGTTTAT TTTTTAAACT   2200

CTGATCTTGA TTGAATGTGA TACCATAAGC ACAGTTAGGC TGCAGTGTAA   2250

ATATATAAAG ACATTGTTCT GAGAGCAGTA CGATTTCATG GAAAGATTGT   2300

TTGGTGGCTT TGTTAAAATT AATAAAGAAT TTTTAAGGAT ATAGTGTAAT   2350

TTTCTTCATT GCATTAATAT AACCAAATAT GCCTACCTAT CTTTGTCTTG   2400

AACCAAATGA ATAGATTTGG AATACTTTAT TGTAATTGAA TTTGATATAA   2450
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AGTTGACTGA GCATTTATGT GTTACCTGCA TGCTTCTGGG TGCATTGAAA   2500

TATTTTAACT TTTAAAATGA TACTATGTTG TTTCAATTTT GACTACCTTT   2550

TGTGAGGCAT ACTGGCTACC TCCTCCTATT AGCTAAGATC TTCCAAAGCC   2600

TTATAATGAA AAGTTTATAT AAACCATTTC TCTTTCAAAT CACTGTCATA   2650

CTTGGTCACG GATCCCAGGA ATATTGTAAA TTTTCTAATT TACTCTGCAC   2700

TTTGTATATC CAGCCTCTAT TACCCTCAAG GTGAATATAA AACTATGTCT   2750

TTTGAATATT TCTCTTTGAT TTTGTGATAG CAGTCCCTCA TATCTTGTAC   2800

TAATTTTATG TATATGTCAA CAGTGGTTGG TCTTTAAAAA TAAATCAAAG   2850

AATAAGTAAA AAAAAAAAAA AAAAAAAAAA AAAAATAAAA AAAAAAAAAA   2900

A   2901

(2)   INFORMATION FOR SEQUENCE ID NO: 5:

      (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 626 amino acids
            (B)   TYPE: amino acid
            (C)   STRANDNESS: single
            (D)   TOPOLOGY: linear

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
1   5   10   15

Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
            20   25   30

Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
        35   40   45

Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
    50   55   60

Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
65   70   75   80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln

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        85   90   95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
           100   105   110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
           115   120   125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
    130   135   140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
145   150   155   160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
           165   170   175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
           180   185   190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
           195   200   205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
    210   215   220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
225   230   235   240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
           245   250   255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
           260   265   270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
          275   280   285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
    290   295   300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
305   310   315   320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
                325   330   335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
           340   345   350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu

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                355                           360                           365
Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
    370                 375                 380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
385                 390                 395                     400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
                405                 410                 415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
            420                 425                 430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
            435                 440                 445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
    450                 455                 460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
465                 470                 475                     480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
                485                 490                 495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
            500                 505                 510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
        515                 520                 525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
    530                 535                 540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
545                 550                 555                     560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
                565                 570                 575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
            580                 585                 590

Asp Glu Glu Leu Tyr Phe His Ser Leu Tyr Arg Glu Arg Gly Asp Gly
        595             600                 605

Met Glu Lys Thr Gln His Asn Lys Lys Trp Met Ile Ala Ser Cys Ser
    610                 615                 620
```

Arg Leu
625

(2)   INFORMATION FOR SEQUENCE ID NO: 6:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 2323 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: nucleic

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA   50

CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG   100

GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA   150

TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACTG   200

CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACTCGG   250

TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA   300

CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG   350

CACAACAAAC AGAATTGGAA TGGATTTCCT CTCCACCCAG TGGGTGGGAA   400

GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATACCAGGT   450

GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA   500

TTTCTAAAGG CAACGCACAA AGGATTTTTG TAGAATTGAA ATTCACCTTG   550

AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAACTTGCA AGGAAACGTT   600

TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG   650

AAAACCTTTA TGTTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA   700

CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA   750

GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCTTT CAGGATGTAG   800

GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG   850

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ACCATTGTTG AGAACTTAGC TGTCTTTCCA GATACAGTGA CTGGTTCGGA      900

ATTTTCCTCC TTAGTCGAGG TCCGTGGGAC ATGTGTCAGC AGTGCCGAGG      950

AAGAGGCAGA AAATTCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG      1000

CTAGTACCCA TTGGAAAATG CATCTGCAAA GCAGGCTATC AGCAAAAAGG      1050

GGACACTTGC GAACCCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG      1100

ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA      1150

TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC      1200

ACCATACGTT GCATGCACGA GGCCTCCCTC TGCACCACAG AACCTTATTT      1250

TCAATATCAA TCAAACGACT GTAAGTTTGG AATGGAGTCC TCCGGCTGAC      1300

AACGGGGGAA GAAACGATGT CACCTACAGA ATACTGTGTA AGCGGTGCAG      1350

TTGGGAACAG GGAGAATGTG TGCCATGCGG AAGTAACATT GGATACATGC      1400

CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTCAT GGACCTACTT      1450

GCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCGGA      1500

CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGTC      1550

AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG      1600

CGGAGTGTGC AGCTTTCCTG GCAGGAGCCG GAGCATCCCA ATGGAGTCAT      1650

CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT      1700

ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATTAA TAATCTGAAA      1750

CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGCCGGTTA      1800

TGGAAACTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG      1850

GTAAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCTGTCATC      1900

ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTCATGGT      1950

GTTCGGCTTC ATCATTGGAA GAAGGCACTG TGGTTATAGC AAGGCTGACC      2000

AAGAAGGGGA TGAAGAACTC TACTTTCATT CTCTTTACAG GGAAAGGGGA      2050

GACGGGATGG AAAAGACACA GCACAATAAG AAGTGGATGA TTGCATCGTG      2100

CTCTCGTTTG TAGGTCTCTT TTCCTAATCA ACACTATGAT TTTGAAGTAC      2150
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GCGTACACGA AGCAAACGGG AAGAGATAAG GAATTAGCAT TGTGAACCTG   2200

ACTGTAATCC TCTCTTCCGG AAAGAGATGA GATGCTATTG CGATGAGAAT   2250

GTACAACTTG CACCTTGAAA TCTTTTTTGA TAATTAGTGC TCAGGGGAGG   2300

GGGGGGGAAG TAGAGAAAGC AAA   2323

(2)   INFORMATION FOR SEQ ID NO: 7:

      (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 6 amino acids
            (B)   TYPE: amino acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala Ala Thr Ala Ala Ala
                5

(2)   INFORMATION FOR SEQ ID NO: 8:

      (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 6 amino acids
            (B)   TYPE: amino acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Ala Thr Ala Ala Ala
                5

(2)   INFORMATION FOR SEQ ID NO: 9:

      (i)   SEQUENCE CHARACTERISTICS:

                (A)   LENGTH: 6 amino acids
                (B)   TYPE: amino acid
                (C)   STRANDEDNESS: single
                (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: peptide

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 9:

His Arg Asp Leu Ala Ala
                5

(2)   INFORMATION FOR SEQ ID NO: 10:

        (i)   SEQUENCE CHARACTERISTICS:

                (A)   LENGTH: 6 amino acids
                (B)   TYPE: amino acid
                (C)   STRANDEDNESS: single
                (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: peptide

        (ix)   FEATURE:

                (D)   OTHER INFORMATION: Xaa in position 2 is valine
                                           or methionine; Xaa in
                                           position 5 is phenylalanine
                                           or tyrosine.

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Xaa Trp Ser Xaa Gly
                5

(2)   INFORMATION FOR SEQ ID NO: 11:

        (i)   SEQUENCE CHARACTERISTICS:

                (A)   LENGTH: 993 amino acids
                (B)   TYPE: amino acid
                (C)   STRANDEDNESS: single
                (D)   TOPOLOGY: linear

        (ii)   MOLECULE TYPE: peptide

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
 1           5               10              15

Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
            20              25              30

Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
            35              40              45

Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
    50              55              60

Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
65              70              75              80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
            85              90              95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
            100             105             110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
        115             120             125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
    130             135             140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
145             150             155             160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
            165             170             175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
        180             185             190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
        195             200             205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
    210             215             220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
 225                 230             235             240

Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
            245             250             255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
```

260   265   270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
        275   280   285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
    290   295   300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
305   310   315   320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
                325   330   335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
            340   345   350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
        355   360   365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
    370   375   380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
385   390   395   400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
            405   410   415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
            420   425   430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
        435   440   445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
    450   455   460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
465   470   475   480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
            485   490   495

Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
        500   505   510

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
        515   520   525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Ala Thr Ala Val Ser
530   535   540

Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val Val Ala Val Ala Gly
545   550   555   560

Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe Ile Ile Gly Arg Arg
                565   570   575

His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly Asp Glu Glu Leu Tyr
                580   585   590

Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr Ile Asp Pro Glu Thr
            595   600   605

Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe Ala Lys Glu Leu Asp
    610   615   620

Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly
625   630   635   640

Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Gln Arg Asp Val Ala
                645   650   655

Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg
                660   665   670

Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn
        675   680   685

Val Val His Leu Glu Gly Val Val Thr Arg Gly Lys Pro Val Met Ile
    690   695   700

Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp Ala Phe Leu Arg Lys
705   710   715   720

His Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly
                725   730   735

Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met Gly Tyr Val His Arg
            740   745   750

Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys
        755   760   765

Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu Asp Asp Pro Glu Ala
    770   775   780

Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val Arg Trp Thr Ala Pro
785   790   795   800

Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser
        805   810   815

Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr
        820   825   830

Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu Gly Tyr
        835   840   845

Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly Leu His Gln Leu Met
    850   855   860

Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg Pro Lys Phe Glu Gln
865   870   875   880

Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn Pro Ser Ser Leu Lys
            885   890   895

Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser Pro Leu Leu Asp Gln
            900   905   910

Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val Gly Glu Trp Leu Gln
            915   920   925

Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr
    930   935   940

Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile Asp Asp Val Met Ser
945   950   955   960

Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys Ile Met Ser Ser Ile
            965   970   975

Gln Thr Met Arg Ala Gln Met Leu His Leu His Gly Thr Gly Ile Gln
            980   985   990

Val

(2)   INFORMATION FOR SEQ ID NO: 12:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 994 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

(ii)   MOLECULE TYPE: peptide

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile
1   5   10   15

Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu
            20   25   30

Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
        35   40   45

Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
    50   55   60

Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
65   70   75   80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
            85   90   95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
        100   105   110

Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
        115   120   125

Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
    130   135   140

Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
145   150   155   160

Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
            165   170   175

Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
        180   185   190

Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
        195   200   205

Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
    210   215   220

Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
225   230   235   240

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Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
                245             250             255

Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
            260             265             270

Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
            275             280             285

Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
        290             295             300

Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
305             310             315             320

Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
            325             330             335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
            340             345             350

Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
        355             360             365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
370             375             380

Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
385             390             395             400

Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
            405             410             415

Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
            420             425             430

Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
            435             440             445

Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln
    450             455             460

Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr
465             470             475             480

Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys
            485             490             495


Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val
            500             505             510
```

Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro
     515   520   525

Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu
     530   535   540

Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val
545   550   555   560

Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe
          565   570   575

Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly
          580   585   590

Asp Glu Glu Leu Tyr Phe His Cys Thr Lys Thr Tyr Ile Asp Pro Glu
     595   600   605

Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe Ala Lys Glu Leu
     610   615   620

Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly Ala Gly Glu Phe
625   630   635   640

Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Gln Arg Asp Val
          645   650   655

Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg
          660   665   670

Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro
          675   680   685

Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly Lys Pro Val Met
     690   695   700

Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp Ala Phe Leu Arg
705   710   715   720

Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg
          725   730   735

Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met Gly Tyr Val His
          740   745   750

Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys
          755   760   765

Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu Asp Asp Pro Glu
     770   775   780

```
Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val Arg Trp Thr Ala
785             790             795                         800

Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp
            805             810                 815

Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro
            820             825             830

Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu Gly
        835             840             845

Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly Leu His Gln Leu
    850             855             860

Met Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg Pro Lys Phe Glu
865             870             875             880

Gln Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn Pro Ser Ser Leu
            885             890             895

Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser Pro Leu Leu Asp
        900             905             910

Gln Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val Gly Glu Trp Leu
        915             920             925

Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly
    930             935             940

Tyr Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile Asp Asp Val Met
945             950             955             960

Ser Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys Ile Met Ser Ser
            965             970             975

Ile Gln Thr Met Arg Ala Gln Met Leu His Leu His Gly Thr Gly Ile
        980             985             990

Gln Val
```